

GenCore version 5.1.4_P5_4578
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OM protein - protein search, using sw model

Run on: May 8, 2003, 14:57:25 ; Search time 96 Seconds
(without alignments)
1446.622 Million cell updates/sec

Title: US-09-462-517-1

Perfect score: 3490
Sequence: 1 MVQFLNGKGTAGELIHMTL.....KVSMEVTRPKPLTEAPKA 674

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3317	95.0	674	5	Q24008
2	3312	94.9	674	5	Q9NBV3
3	2136	61.2	665	5	Q23823
4	544.5	15.6	2042	4	Q75970
5	523	15.0	2055	11	Q8VBX6
6	523	15.0	2055	11	Q8VBX6
7	519	14.9	2055	11	Q921K3
8	519	14.9	2055	11	Q8VBX6
9	508	14.6	2054	11	Q55164
10	490	14.0	1134	4	Q9H3N9
11	427.5	12.2	2208	5	Q09515
12	419	12.0	1552	4	Q60833
13	411	11.8	1582	4	Q43742
14	384	11.0	1524	4	Q15249
15	345.5	9.9	612	11	Q70471
16	253	7.2	1695	5	Q9BKL2

17	246.5	7.1	582	4	Q8WX31	Q8WX31 homo sapien
18	239	6.8	51	5	Q9TWC8	Q9TWC8 calliphora
19	239	6.8	526	11	Q08783	Q08783 mus musculus
20	235	6.7	453	4	Q43798	Q43798 homo sapien
21	231.5	6.6	2460	11	Q64512	Q64512 mus musculus
22	229	6.6	2484	6	Q28006	Q28006 bos taurus
23	221.5	6.3	1163	13	Q9YHW2	Q9YHW2 gallus gall
24	210	6.0	1663	11	Q8V111	Q8V111 mus musculus
25	203	5.8	346	11	Q9CS43	Q9CS43 mus musculus
26	201.5	5.7	871	5	Q9X235	Q9X235 drosophila
27	200.5	5.7	2766	11	Q9QZ88	Q9QZ88 rattus norv
28	199.5	5.7	871	5	Q9NB04	Q9NB04 drosophila
29	199.5	5.7	904	11	Q921G9	Q921G9 mus musculus
30	198.5	5.7	721	11	Q91WJ1	Q91WJ1 mus musculus
31	198.5	5.7	1256	4	Q75085	Q75085 homo sapien
32	198	5.7	346	4	Q8WU78	Q8WU78 homo sapien
33	196	5.6	944	11	Q922S3	Q922S3 mus musculus
34	193.5	5.5	1287	4	Q96029	Q96029 homo sapien
35	193	5.5	1462	4	Q96027	Q96027 homo sapien
36	191	5.5	1564	4	Q14160	Q14160 homo sapien
37	191	5.5	1630	4	Q8WVW8	Q8WVW8 homo sapien
38	190.5	5.5	1179	11	Q9JK71	Q9JK71 rattus norv
39	189.5	5.4	1114	11	Q9R271	Q9R271 rattus norv
40	189.5	5.4	1126	11	Q9EQ39	Q9EQ39 mus musculus
41	189.5	5.4	1277	11	Q88382	Q88382 rattus norv
42	184.5	5.3	632	4	Q8BY20	Q8BY20 homo sapien
43	184.5	5.3	728	4	Q8TB81	Q8TB81 homo sapien
44	182.5	5.2	687	11	Q91XL2	Q91XL2 mus musculus
45	182.5	5.2	960	5	Q9VYZ5	Q9VYZ5 drosophila

ALIGNMENTS

RESULT 1	ID	Q24008	PRELIMINARY:	PRT:	674 AA.
AC	Q24008	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)				
DR	01-JUN-2001 (TREMBLrel. 17, Last annotation update)				
OC	INAD protein.				
DE	INAD OR CG3504.				
OS	Drosophila melanogaster (Fruit fly).				
CC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
CC	Ephydroidea; Drosophilidae; Drosophila.				
OX	NCBI_TaxID=7227;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-BERKELEY;				
RX	MEDLINE-20196006; PubMed-10731132;				
RA	Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,				
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,				
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,				
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,				
RA	Brandon R.C., Rogers Y.-H.C., Blake J.R.G., Champagne M., Pfeiffer B.D.,				
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,				
RA	Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,				
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,				
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,				
RA	Borrova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,				
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,				
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,				
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,				
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,				
RA	Durkin K.J., Evangelista C.C., Ferraz C., Gerbasi S., Fleischmann W.,				
RA	Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,				
RA	Glocke A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,				
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,				
RA	Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,				
RA	Jaislin M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,				
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,				

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mallet B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merulov G., Milshina N.V., Mobarry C., Morris J., Mosher A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.H., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Pui V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos K., Simpson M., Skupski M.P., Smith T.,
 RA Spletter E., Spreading A.C., Stapleton M., Strong R., Sun E.,
 RA Svitskay R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RT "The genome sequence of *Drosophila melanogaster*.";
 RT Science 287:2185-2195 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-COMPOUND EYE;
 RA Lindsley D.L., Zimm G.G.;
 RT "The genome of *Drosophila melanogaster*.";
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-COMPOUND EYE;
 RX MEDLINE-95127229; PubMed-7826638;
 RA Shieh B.H., Niemeyer B.;
 RT "A novel protein encoded by the *Inad* gene regulates recovery of visual
 RT transduction in *Drosophila*.";
 RL Neuron 14:201-210 (1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE-COMPOUND EYE;
 RA Shieh B.;
 RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE-COMPOUND EYE;
 RA Shieh B.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE003458; AAF46915.1;
 DR EMBL: U15803; AAC36490.1;
 DR HSSP: P31016; 1BFE.
 DR FlyBase: FBgn0001263; *Inad*.
 DR InterPro: IPR001478; PDZ.
 DR Pfam: PF00595; PDZ: 5.
 DR SMART: SM00228; PDZ: 5.
 DR PROSITE: PS50106; PDZ: 5.
 SQ SEQUENCE 674 AA; 74332 MW; D4C24091D99EA7F3 CRC64;
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 Best Local Similarity 95.3%; Pred. No. 2.5e-200;
 Matches 654; Conservative 1; Mismatches 7; Indels 24; Gaps 3;
 QY 1 MVQFLGKGTAGELIHMTLDKTKGKSGICIVRGVDSPTKTTGIFINGIYVDSPAH 60
 DB 1 MVQFLGKGTAGELIHMTLDKTKGKSGICIVRGVDSPTKTTGIFINGIYVDSPAH 60
 QY 1 CGRLKVGDRILSLNGKVRNSTEAVIDLKKEADFKLEIQTDFKSDDEQAKSDPSRN 120
 DB 1 CGRLKVGDRILSLNGKVRNSTEAVIDLKKEADFKLEIQTDFKSDDEQAKSDPSRN 120
 QY 121 GYMAKKNFNEQTTNNASGGGOGGOGGOGGAGNRRQOSMOKRNTTFTASRKH 180
 DB 121 GYMAKKNFNEQTTNNASGGGOGGOGGOGGAGNRRQOSMOKRNTTFTASRKH 180
 QY 181 NYADEDEDTFDMTGRIRTEAGYEIDRASAGCNKLNKOEKDRDEDEDFGYTAAKINR 240
 DB 181 NYADEDEDTFDMTGRIRTEAGYEIDRASAGCNKLNKOEKDRDEDEDFGYTAAKINR 240
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 DB 241 YNMKKDLRIEVRDASKPLGLALAGHKDRKAKCFVAGVDPNGLSGVDIKPDDEIVEY 300

DB 241 YNMKKDLRIEVRDASKPLGLALAGHKDRKAKCFVAGVDPNGLSGVDIKPDDEIVEY 300
 QY 301 NGVVLKRNCHLNASAVFKNVDGKLVIATISRRKPNDEGMCVKPKIKFPASDETFIFDQ 360
 DB 301 NGVVLKRNCHLNASAVFKNVDGKLVIATISRRKPNDEGMCVKPKIKFPASDETFIFDQ 360
 QY 361 FPKARFVQVKEEFLIMVYTGKHAEGSGIFISDRLREGSNALACVYCDMLANOVY 420
 DB 361 FPKARFVQVKEEFLIMVYTGKHAEGSGIFISDRLREGSNALACVYCDMLANOVY 420
 QY 421 TLESNDDATGLKRAEGVVTMLTLKSEAIAKAEKKEEKEEKEEKEEKEEKEEKEE 480
 DB 421 TLESNDDATGLKRAEGVVTMLTLKSEAIAKAEKKEEKEEKEEKEEKEEKEEKEE 480
 QY 481 EIRPNKKILIELKVEKPKMCHLRKOKOPCHDWLC---NPRLS-----GGQVAA 528
 DB 481 EIRPNKKILIELKVEKPKMCHLRKOKOPCHDWLC---NPRLS-----GGQVAA 528
 QY 529 DKRLKIFDHIDINGTPIHVGSMITLVHQLPHTTEKAVTLTVFRADPELEKFNVDLM 588
 DB 529 DKRLKIFDHIDINGTPIHVGSMITLVHQLPHTTEKAVTLTVFRADPELEKFNVDLM 588
 QY 589 KRAGKELGLSLSPNEIGCTIADLIQGYPEIDSKLORGDIITFKNGDALEGLFPQYCYAL 648
 DB 589 KRAGKELGLSLSPNEIGCTIADLIQGYPEIDSKLORGDIITFKNGDALEGLFPQYCYAL 648
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 DB 649 FKGANCKVSMETTRPPTLRTPEPKA 674
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 AC Q9NBV3;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE *INAD*.
 GN *INAD* OR CG3504.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; *Drosophila*.
 OX NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CANTON-S;
 RA Ashari M., Shieh B.;
 RT "The *Inad* locus in *Drosophila*.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF245280; AAF81203.1;
 DR HSSP: P31016; 1BFE.
 DR FlyBase: FBgn0001263; *Inad*.
 DR InterPro: IPR001478; PDZ.
 DR Pfam: PF00595; PDZ: 5.
 DR SMART: SM00228; PDZ: 5.
 DR PROSITE: PS50106; PDZ: 5.
 SQ SEQUENCE 674 AA; 74305 MW; 55B1C57B7A100FID CRC64;
 Query Match 94.9%; Score 3312; DB 5; Length 574;
 Best Local Similarity 95.2%; Pred. No. 5.1e-200;
 Matches 653; Conservative 2; Mismatches 7; Indels 24; Gaps 3;
 QY 1 MVQFLGKGTAGELIHMTLDKTKGKSGICIVRGVDSPTKTTGIFINGIYVDSPAH 60
 DB 1 MVQFLGKGTAGELIHMTLDKTKGKSGICIVRGVDSPTKTTGIFINGIYVDSPAH 60
 QY 61 CGRLKVGDRILSLNGKVRNSTEAVIDLKKEADFKLEIQTDFKSDDEQAKSDPSRN 120
 DB 61 CGRLKVGDRILSLNGKVRNSTEAVIDLKKEADFKLEIQTDFKSDDEQAKSDPSRN 120
 QY 121 GYMAKKNFNEQTTNNASGGGOGGOGGOGGAGNRRQOSMOKRNTTFTASRKH 180
 DB 121 GYMAKKNFNEQTTNNASGGGOGGOGGOGGAGNRRQOSMOKRNTTFTASRKH 180

GenCore version 5.1.4-p5_4578
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OK protein - protein search, using sw model

Run on: May 8, 2003, 14:57:17 ; Search time 40 Seconds
(without alignments)
2245.273 Million cell updates/sec

Title: US-09-462-517-1

Perfect score: 3490
Sequence: 1 MWQFLGKQGTAGELIHVTL.....KVSMEVTRPKPLTEAPKA 674

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Genesec 101002:*

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22: /SIDS2/gcgcdata/geneseq/geneseqp-emb1/AA2001.DAT:*
23: /SIDS2/gcgcdata/geneseq/geneseqp-emb1/AA2002.DAT:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3490	100.0	674	20	AAW92953
2	3317	95.0	674	22	ABBS9957
3	539	15.4	1111	23	AAU87918
4	537	15.4	2037	21	AAV53753
5	533.5	15.3	2070	20	AAV04733
6	523.5	15.0	856	21	AAU01383
7	508	14.6	1373	20	AAV04730
8	508	14.6	2000	20	AAV04732
9	505.5	14.5	1005	20	AAV04731
10	491	14.1	1881	20	AAV24025

11	460	13.2	1627	22	ABG06117	Novel: human diapo
12	446.5	12.8	763	20	AAV04741	PDZ domain-contain
13	419	12.0	1552	22	AAW78793	Human protein SEQ
14	419	12.0	1554	22	ABG07288	Novel: human diapo
15	411	11.8	1584	22	ABG07290	Novel: human diapo
16	384	11.0	1526	22	ABG06116	Novel: human diapo
17	384	11.0	1526	22	ABG07289	Novel: human diapo
18	384	11.0	1526	22	AAW79777	Human protein SEQ
19	241.5	6.9	2485	21	AAV19343	Amlyc acid sequenc
20	238.5	6.8	2466	16	AAW71498	Human protein tyro
21	238.5	6.8	2466	21	AAV75999	Intracellular proto
22	238.5	6.8	2466	21	AAV90272	Human PTPBL phosph
23	228	6.3	206	20	AAV74151	Human prostate tum
24	220	6.3	318	20	AAV74150	Human prostate tum
25	209.5	6.0	1239	20	AAV04734	Protein containing
26	206.5	5.9	354	23	AAU87920	Human PDZ3 protei
27	201.5	5.8	871	22	ABBS7855	Drosophila melanog
28	201.5	5.8	871	22	ABBS7265	Drosophila melanog
29	200.5	5.7	928	23	AAE21718	Human PKIN-13 prot
30	200.5	5.7	1037	22	ABG22366	Novel: human diapr
31	199	5.7	724	23	ABBS04799	LDL receptor blind
32	196.5	5.6	724	23	ABBS04798	LDL receptor blind
33	196.5	5.6	767	21	AAU82138	Human post-synapti
34	196.5	5.6	767	23	AAU84269	Human endometrial
35	196.5	5.6	767	23	AAU84328	Human protein cont
36	191	5.5	1535	23	AAU87934	Rat synaptic scaff
37	189.5	5.4	1277	21	AAU80149	Neuron-associated
38	188.5	5.4	632	21	AAU801385	Human polyptide,
39	186.5	5.3	304	22	AAW93296	PDZ encoded domain
40	185	5.3	344	22	ABBS5834	Human post-synapti
41	185	5.3	344	22	ABBS7623	Human post-synapti
42	185	5.3	344	22	ABBS5035	Human post-synapti
43	184.5	5.3	469	22	AAU40870	Human polyptide
44	184.5	5.3	590	20	AAV04736	PDZ domain-contain
45	184.5	5.3	632	21	AAV66689	Membrane-bound pro

ALIGNMENTS

RESULT 1	AAW92953	standard: Protein; 674 AA.
AC	AAW92953;	
XX		
AC	14-MAY-1999	(first entry)
XX		
DE	Fly transducisome Inad protein.	
XX		
KW	Inad; transducisome; fly; insect; signal transduction protein; mutant;	
KW	PDZ domain; modulator; cell surface receptor; ion channel; treatment;	
XX	disorder.	
OS	Insecta.	
XX		
FT	Key	Location/Qualifiers
FT	Misc-difference 319	/note- "encoded by AGC"
FT	Misc-difference 501	/note- "Encoded by GT"
FT	Misc-difference 508	/note- "Encoded by GAA"
FT	Misc-difference 524	/note- "Encoded by GGA"
FT		
XX	W09903974-A1.	
XX		
PD	28-JAN-1999.	
XX		
PF	15-JUL-1998;	98MO-US14667.
XX		
PR	15-JUL-1997;	97US-0052588.

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattle J., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Meruliov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Nelson S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Neufeld D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheller F., Shen H.,
 RA Shie B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [12]
 RP SEQUENCE FROM N.A.
 RC TISSUE-COMPOUND EYE.
 RA Lindsley D.L., Zimm G.G.;
 RT "The genome of *Drosophila melanogaster*.";
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 RN [13]
 RP SEQUENCE FROM N.A.
 RC TISSUE-COMPOUND EYE.
 RX MEDLINE-95127229; PubMed-7826638;
 RA Shieh B.H., Niemeyer B.;
 RT "A novel protein encoded by the *Inad* gene regulates recovery of visual
 RL transduction in *Drosophila*.";
 RL Neuron 14:201-210(1995).
 RN [14]
 RP SEQUENCE FROM N.A.
 RC TISSUE-COMPOUND EYE.
 RA Shieh B.;
 RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
 RN [15]
 RP SEQUENCE FROM N.A.
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 RA Shieh B.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AEO03458; AAF46915.1;
 DR EMBL: U15803; AAC36490.1;
 DR HSSP: P31016; 1BFE.
 DR Flybase: FBgn0001263; *Inad*.
 DR InterPro: IPR001478; PDZ.
 DR Pfam: PF00595; PDZ; 5.
 DR SMART: SM00228; PDZ; 5.
 DR PROSITE: PS50106; PDZ; 5.
 SQ SEQUENCE 674 AA; 74332 MW; D4C24091D99EATF3 CRC64;

Query Match 95.0%; Score 3317; DB 5; Length 674;
 Best Local Similarity 95.3%; Pred. No. 2.5e-200;
 Matches 654; Conservative 1; Mismatches 7; Indels 24; Gaps 3;

OY 1 MVQFLKQGTAGELIHVTLDTKTKKSGFGICIRGEVKNDSPTNTTGTGIFKIGVPSPAH 60
 DB 1 MVQFLKQGTAGELIHVTLDTKTKKSGFGICIRGEVKNDSPTNTTGTGIFKIGVPSPAH 60
 OY 61 LCGRLKVGRIILSLNKDVRNSTEQAVIDLKREADFKELEIOTFDFKSDQQAQSDPSRN 120
 DB 61 LCGRLKVGRIILSLNKDVRNSTEQAVIDLKREADFKELEIOTFDFKSDQQAQSDPSRN 120
 OY 121 GYVQAKNKNFNOGTNNNNSGGGGMGGGGMGGGMNROSGMOKRNTFTTSMOKHS 180
 DB 121 GYVQAKNKNFNOGTNNNNSGGGGMGGGGMGGGMNROSGMOKRNTFTTSMOKHS 180
 OY 181 NTADEDEDEPTDMTGRIRTEAGYEIDRASGKCKLKOEDRDKDEDEFGYTMATINKR 240
 DB 181 NTADEDEDEPTDMTGRIRTEAGYEIDRASGKCKLKOEDRDKDEDEFGYTMATINKR 240
 OY 241 YNMKDLRIEVOBRSKPLGLAGHKDROKACPVACVDPNGALGSVDIKGDEIVEY 300
 DB 241 YNMKDLRIEVOBRSKPLGLAGHKDROKACPVACVDPNGALGSVDIKGDEIVEY 300

DB 241 YNMKDLRIEVOBRSKPLGLAGHKDROKACPVACVDPNGALGSVDIKGDEIVEY 300
 OY 301 NNNVTLKRNCHLASAVFNVDCKLVMTSRKRPNDGNCVPRIKFPASDETFEFDQ 360
 DB 301 NNNVTLKRNCHLASAVFNVDCKLVMTSRKRPNDGNCVPRIKFPASDETFEFDQ 360
 OY 361 NNNVTLKRNCHLASAVFNVDCKLVMTSRKRPNDGNCVPRIKFPASDETFEFDQ 360
 DB 361 NNNVTLKRNCHLASAVFNVDCKLVMTSRKRPNDGNCVPRIKFPASDETFEFDQ 360
 OY 361 FPKATVOYRKGEFGIMVITGKHAEVGSGIFISDLRESNMLGVYGMULAVNDV 420
 DB 361 FPKATVOYRKGEFGIMVITGKHAEVGSGIFISDLRESNMLGVYGMULAVNDV 420
 OY 421 TLESNYDATGILKRAEGVWITLLTJLSEENIAKAEKKEEKEEKEEKEEKEEKEE 480
 DB 421 TLESNYDATGILKRAEGVWITLLTJLSEENIAKAEKKEEKEEKEEKEEKEEKEE 480
 OY 481 EKKPKKTLIELKVKKKRMGCHRLRQOPCHMCL-----NHPRLS-----GGVAA 528
 DB 481 EKKPKKTLIELKVKKKRMGCHRLRQOPCHMCL-----NHPRLS-----GGVAA 528
 OY 481 EKKPKKTLIELKVKKKRMGCHRLRQOPCHMCL-----NHPRLS-----GGVAA 528
 DB 481 EKKPKKTLIELKVKKKRMGCHRLRQOPCHMCL-----NHPRLS-----GGVAA 528
 OY 529 DKRLKIFDHIDINCTPIVGSMTLKVHOLEFHTYERAVTLTVFRADPELEKPNVLM 588
 DB 529 DKRLKIFDHIDINCTPIVGSMTLKVHOLEFHTYERAVTLTVFRADPELEKPNVLM 588
 OY 529 DKRLKIFDHIDINCTPIVGSMTLKVHOLEFHTYERAVTLTVFRADPELEKPNVLM 588
 DB 529 DKRLKIFDHIDINCTPIVGSMTLKVHOLEFHTYERAVTLTVFRADPELEKPNVLM 588
 OY 589 KKAGKEGLSLSPNEIGCTIADLIQGYPEIDSKLQRGDIITKFGDLEGLPEOVYAL 648
 DB 589 KKAGKEGLSLSPNEIGCTIADLIQGYPEIDSKLQRGDIITKFGDLEGLPEOVYAL 648
 OY 649 FKANGKSMVEVTRPKPLTRTEAPRA 674
 DB 649 FKANGKSMVEVTRPKPLTRTEAPRA 674

RESULT 2
 O9NBV3 PRELIMINARY; PRT: 674 AA.
 AC O9NBV3;
 DT 01-OCT-2000 (TREMREL. 15, Created)
 DT 01-OCT-2000 (TREMREL. 15, Last sequence update)
 DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
 DE INAD.
 GN INAD OR CG3504.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Terebrata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; *Drosophilidae*; *Drosophila*.
 OX NCBL_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CANTON-S;
 RA Ashari M., Shieh B.;
 RT "The *Inad* locus in *Drosophila*.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AAF45280; AAF81203.1;
 DR HSSP: P31016; 1BFE.
 DR Flybase: FBgn0001263; *Inad*.
 DR InterPro: IPR001478; PDZ.
 DR Pfam: PF00595; PDZ; 5.
 DR SMART: SM00228; PDZ; 5.
 DR PROSITE: PS50106; PDZ; 5.
 SQ SEQUENCE 674 AA; 74305 MW; 55B1C57B7A10E1D CRC64;

Query Match 94.9%; Score 3312; DB 5; Length 674;
 Best Local Similarity 95.2%; Pred. No. 5.1e-200;
 Matches 653; Conservative 2; Mismatches 7; Indels 24; Gaps 3;

OY 1 MVQFLKQGTAGELIHVTLDTKTKKSGFGICIRGEVKNDSPTNTTGTGIFKIGVPSPAH 60
 DB 1 MVQFLKQGTAGELIHVTLDTKTKKSGFGICIRGEVKNDSPTNTTGTGIFKIGVPSPAH 60
 OY 61 LCGRLKVGRIILSLNKDVRNSTEQAVIDLKREADFKELEIOTFDFKSDQQAQSDPSRN 120
 DB 61 LCGRLKVGRIILSLNKDVRNSTEQAVIDLKREADFKELEIOTFDFKSDQQAQSDPSRN 120
 OY 121 GYVQAKNKNFNOGTNNNNSGGGGMGGGGMGGGMNROSGMOKRNTFTTSMOKHS 180
 DB 121 GYVQAKNKNFNOGTNNNNSGGGGMGGGGMGGGMNROSGMOKRNTFTTSMOKHS 180